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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=4; day=15; hr=13; min=10; sec=12; ms=469;]

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Application No: 10532681 Version No: 2.0

Input Set:

Output Set:

Started: 2010-04-07 18:29:50.513
Finished: 2010-04-07 18:29:53.866
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 353 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2010-04-07 18:29:50.513
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Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 353 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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SEQUENCE LISTING

<110> LUKYANOV, SERGEY A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10532681

<141> 2010-04-07

<160> 23

<170> PatentIn version 3.4

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<211> 784

<212> DNA

<213> Phialidium sp.

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gtccatgtcc ctgaatacca tcataaca taccatgtca ctctcagcaa agatgttact 660

gatcacaggg ataacatgag ctgggtgaa accgtacggg ctgtggattg cagaaaaaca 720

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784

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<211> 234

<212> PRT

<213> Phialidium sp.

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu

225 230

<210> 3

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

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aaagttgtatg cccaaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttgcacaaat atggtccaga attaaaggat 240

ttctacaaga gttgcattgcc tgaaggctat gtgcaggagc gtacaatcac atttgaagg 300

gacggagttat ttaaaactcg cgctgaagtt acatttggaa acggatctgt ttataaccga 360

gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttgaaa gaatcttcaa 420

ttcaatttca cacctcatttgc tctttacatt tggggagatc aggctaatac tggtttgaag 480

tctgcatttca aaattatgca ttagattact ggtcaaaag gagacttcat tgttgcagac 540

cacacccaaa tgaacacacc catgggtggt ggaccagtcc atgtccctga ataccatcat 600

atgacataacc atgtcactct cagcaaagat gttactgatc acagggataa catgagctt 660

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<210> 4

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val

1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys

20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<211> 705

<212> DNA

<213> Artificial sequence

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<223> phiYFP-M0 mutant of the phiYFP

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aaagttgtatg cccaaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttgcacaaat atggtccaga attaaaggat 240
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gacggaaaact taaaactcg cgctgaagtt acatttggaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg attaagaaa gacggacatg tgcttgaaa gaatcttcaa 420
ttcaatttca cacctcatttgc ttttacatt tggggagatc aggctaatac tggtttgaag 480
tctgctttca aaattcgcca ttagattact ggtcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc catgggtggt ggaccagtcc atgtccctga aaaccatcat 600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagctt 660
aaggaaaccg tacgggctgt ggattgcaga aaaacatatac tttaa 705

<210> 6
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp

65

70

75

80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 7

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aaagttgatg cccattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttgcacaaat atggccaga attaaaggat 240
ttctacaaga gttgcattgcc tgatggctat gtgcaggagc gtacaatcac atttgaagg 300
gacggaaaact taaaactcg cgctgaagtt acatttggaaa acggatctgt ttataaccga 360
gtcaaactta atggacaagg attaagaaa gacggacatg tgcttgaaa gaatcttga 420
tcaatttca cacctcattt tctttacatt tggggagatc aggtaatca tggtttgaag 480
tctgctttca aaatttgcca ttagattact gcatcaaaag gagacttcat tgttgcagac 540
cacacccaaa tgaacacacc cattgggtggt ggaccagtcc atgtccctga ataccatcat 600
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aaggaaaccg tacgggctgt ggattgcaga aaaacatatac tttaa 705

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<211> 234
<212> PRT
<213> Artificial sequence

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<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> humanized version of the phiYFP-M1

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aaggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcacctg 180
tggaccaccc tgacctacgg cgccccagtgc ttcgccaagt acggccccga gctgaaggat 240
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gatggcaatt tcaagacccg cgcccgagggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctggcaa gaatctggag 420
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cacacccaga tgaataacccc catcgccggc ggccccgtgc acgtgcccga gtaccaccac 600
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<210> 10
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> humanized version of the phiYFP-M1

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys

145

150

155

160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<213> Anthomedusae species

<220>
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<223> hydromedusa 1 from sub-order Anthomedusae

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gcaatgacag aaacatttca gaaaaatttgc ccatataagt tagaatttgc tgtagatgtt 240
gatggccaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgttaatt 300
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gttttagaaa cagcagctaa aattactatg gaaagtggtg caatagtcaa tagaataaaat 540
gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatccccc 600
cctcccttcga caacatatgt tttccccgag ggagaaggta ttcgaatcat ctatagaaac 660
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tttgacgctg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaaag	900
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<213> Anthomedusae species